

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 18:26:51 ; Search time 7218 Seconds
(without alignments)
11305.662 Million cell updates/sec

Title: US-10-023-782A-3
Perfect score: 2804
Sequence: 1 tcgcagagccgcgcgatgcgt.....gaaaaaaaaaaaaaaaaa 2804

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	30.4	1.1	49 6	AX099434	AX099434 Sequence
2	30	1.1	45 6	AX287571	AX287571 Sequence
3	30	1.1	45 6	AX287575	AX287575 Sequence
4	29.2	1.0	43 6	AX225198	AX225198 Sequence
5	29.2	1.0	50 6	AX261361	AX261361 Sequence
c 6	29.2	1.0	50 6	I36502	I36502 Sequence 1
7	29	1.0	46 6	AX287578	AX287578 Sequence
8	29	1.0	46 6	AX287582	AX287582 Sequence
c 9	28.8	1.0	45 6	E50989	E50989 Method for
c 10	28.4	1.0	40 6	A48799	A48799 Sequence 6
11	28.4	1.0	46 6	AX287579	AX287579 Sequence
12	28.4	1.0	46 6	AX287583	AX287583 Sequence
13	28	1.0	37 6	AX106972	AX106972 Sequence
c 14	28	1.0	37 6	I29931	I29931 Sequence 44
15	27.8	1.0	43 6	AX443022	AX443022 Sequence
16	27.8	1.0	43 6	AX459616	AX459616 Sequence
17	27.8	1.0	44 6	AX206861	AX206861 Sequence
c 18	27.6	1.0	44 6	AR038858	AR038858 Sequence
c 19	27.6	1.0	49 11	G73668	G73668 RZ220R etio
20	27.4	1.0	38 6	E50766	E50766 Vector expr
21	27.4	1.0	49 3	DDU63607	DDU63607 Dictyosteli
22	27.4	1.0	50 6	I23510	I23510 Sequence 5
23	27.4	1.0	50 6	I28359	I28359 Sequence 5
24	27.4	1.0	50 6	I28514	I28514 Sequence 5
25	27.4	1.0	50 6	I41125	I41125 Sequence 5
26	27.4	1.0	50 6	I49056	I49056 Sequence 5
27	27.4	1.0	50 6	I70295	I70295 Sequence 5
28	27.4	1.0	50 6	I90068	I90068 Sequence 5
29	27.2	1.0	33 6	BD011883	BD011883 Detection
30	27.2	1.0	33 23	BD004363	BD004363 Detection
31	27.2	1.0	42 6	I32405	I32405 Sequence 2
c 32	27.2	1.0	47 6	AX458031	AX458031 Sequence
c 33	27.2	1.0	48 6	AX166869	AX166869 Sequence
c 34	26.8	1.0	44 6	I29927	I29927 Sequence 40
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40	26	0.9	34 6	A63578	A63578 Sequence 19
41	26	0.9	45 6	AX287570	AX287570 Sequence
42	26	0.9	45 6	AX287574	AX287574 Sequence
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44	25.8	0.9	48 6	AR043404	AR043404 Sequence
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ALIGNMENTS

RESULT 1
AX099434/c 49 bp DNA linear PAT 02-APR-2001
LOCUS AX099434
DEFINITION Sequence 74 from Patent WO0119988.
ACCESSION AX099434
VERSION AX099434.1 GI:13538544
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 49)
Jacobs,K., Mccoy,J.M., Lavallie,E.R., Collins-Racie,L.A., Evans,C.,
Merberg,D., Treacy,M., Bowman,M.R., Spaulding,V. and Agostino,M.J.
Secreted proteins and polynucleotides encoding them

JOURNAL	Patent: WO 0119988-A 74 22-MAR-2001;
FEATURES	Genetics Institute, Inc. (US)
source	Location/Qualifiers 1. .49 /organism="Homo sapiens" /db_xref="taxon:9606"
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Db	49 TTTTTCCTTAATTTTTTTTTTTTTTTTNTTAAATT 1
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LOCUS	AX287571 45 bp DNA linear PAT 21-NOV-2001
DEFINITION	Sequence 14 from Patent WO0177390.
ACCESSION	AX287571
VERSION	AX287571.1 GI:17049337
KEYWORDS	.
SOURCE	synthetic construct. synthetic construct artificial sequences.
ORGANISM	1
REFERENCE	abarz A,P. Process for allele discrimination utilizing primer extension
AUTHORS	Patent: WO 0177390-A 14 18-OCT-2001;
TITLE	Molecular
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OY	2155 TTTTTCCTCTTTTTTTTTTTTAACTTT 2192
Db	4 TTTTTCCTTAATTTTTTTTTTTTCACTT 41
RESULT 3	
LOCUS	AX287575 45 bp DNA linear PAT 21-NOV-2001
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VERSION	AX287575.1 GI:17049341
KEYWORDS	.
SOURCE	synthetic construct. synthetic construct artificial sequences.
ORGANISM	1
REFERENCE	abarz A,P. Process for allele discrimination utilizing primer extension
AUTHORS	Patent: WO 0177390-A 18 18-OCT-2001;
TITLE	Molecular
JOURNAL	location/Qualifiers 1. .45 /organism="synthetic construct" /db_xref="taxon:32630" /note="P1 primer for use in allele discrimination"
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Dn	4 TTTTTCCTCCTTTTTTTTTTTCACTT	41					
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	LOCUS AX225198	43 bp	DNA	linear	PAT 10-SEP-2001		
	DEFINITION Sequence 7 from Patent WO0161033.						
	AX225198						
	VERSION AX225198.1 GI:15555219						
	KEYWORDS . synthetic construct.						
SOURCE	synthetic construct artificial sequences.						
ORGANISM	1 (bases 1 to 43)						
REFERENCE	Schouten,J.P.						
AUTHORS	Multiplex ligatable probe amplification						
JOURNAL	Patent: WO 0161033-A 7 23-AUG-2001; Schouten, Johannes Petrus (NL) Location/Qualifiers						
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Dn	1 TTTTTCCTCTTTTAAAAAAAAGTTT	42					
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	RESULT 5						
	LOCUS AX261361	50 bp	DNA	linear	PAT 26-OCT-2001		
	DEFINITION Sequence 1012 from Patent WO0173027.						
	AX261361						
	ACCESSION AX261361.1 GI:16510328						
VERSION	. human.						
KEYWORDS	Homo sapiens						
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ORGANISM	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.						
REFERENCE	1 Meagher,M.J., Xu,J. and King,G.E.						
AUTHORS	Compositions and methods for therapy and diagnosis of colon cancer						
JOURNAL	Patent: WO 0173027-A 1012 04-OCT-2001; CORIXA CORPORATION (US) Location/Qualifiers						
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Dn	1 TTTTTCCTCTTTTAAAAAAAAGTTT	42					

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 17:59:45 ; Search time 595 Seconds
(without alignments)
10612.779 Million cell updates/sec

Title: US-10-023-782A-3
Perfect score: 2804
Sequence: 1 tcgcagagccgcgcgatgcgt.....gaaaaaaaaaaaaaaaaa 2804

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	31.4	1.1	47	22	AAU07489	Human reproductive
C 2	31.4	1.1	50	22	AAU28562	Human SNP oligonuc
C 3	30.6	1.1	48	16	AAT04081	Trypsin inhibitory
C 4	30.4	1.1	49	19	AAV41447	Nucleotide sequenc
C 5	30.4	1.1	49	22	AAF98419	Human cDNA clone B
C 6	30	1.1	45	24	AAS95724	Allele discriminat
C 7	30	1.1	45	24	AAS95728	Allele discriminat
C 8	29.8	1.1	50	24	ABK30194	CYP2D6 gene polymo
C 9	29.6	1.1	50	19	AAV37933	Primer of the spec

C 10	29.2	1.0	43	22	AAD17216	Human mRNA hybridi
C 11	29.2	1.0	44	19	AAV09273	Nucleotide sequenc
C 12	29.2	1.0	49	18	AAT88080	3' portion of cDNA
C 13	29.2	1.0	49	18	AAV02146	Human secreted pro
C 14	29.2	1.0	50	15	AAQ66922	Poly-da 50mer prob
C 15	29.2	1.0	50	22	AAF60897	Conjugate forming
C 16	29.2	1.0	50	23	AAS58336	CDNA #1012 encodin
C 17	29.2	1.0	50	24	ABN89414	Polymorphism detec
C 18	29	1.0	38	22	AAU07488	Human reproductive
C 19	29	1.0	46	24	AAS95731	Allele discriminat
C 20	29	1.0	46	24	AAS95735	Allele discriminat
C 21	28.8	1.0	43	22	AAU31948	Human SNP oligonuc
C 22	28.8	1.0	45	22	AAF26960	Primer for amplify
C 23	28.4	1.0	40	13	AAQ25031	Oligonucleotide sp
C 24	28.4	1.0	40	21	AAA39649	Primer used in con
C 25	28.4	1.0	46	24	AAS95732	Allele discriminat
C 26	28.4	1.0	46	24	AAS95736	Allele discriminat
C 27	28.2	1.0	36	24	AAD27117	RNA template, AU u
C 28	28.2	1.0	37	24	AAD27125	CYP2D6 gene polymo
C 29	28.2	1.0	47	24	ABK30186	Human SGP28 cDNA s
C 30	28	1.0	44	22	AAU30581	Example PCR primer
C 31	28	1.0	48	22	AAS04299	Hepatoma AS-30D Ty
C 32	28	1.0	49	18	AAT80510	DNA synthesis prim
C 33	27.8	1.0	42	21	AAA37946	CDNA synthesis pri
C 34	27.8	1.0	43	21	AAA09164	Oligonucleotide DP
C 35	27.8	1.0	43	21	AAA14804	Primer used for ge
C 36	27.8	1.0	43	21	AAZ93041	CDNA synthesis pri
C 37	27.8	1.0	43	21	AAZ94895	CDNA synthesis pri
C 38	27.8	1.0	43	21	AAZ94401	Human SGP28 cDNA s
C 39	27.8	1.0	43	22	AAD06225	RT primer, SEQ ID
C 40	27.8	1.0	43	22	AAF76005	Human secreted tum
C 41	27.8	1.0	43	22	AAD04804	Human 83p2H3 cDNA
C 42	27.8	1.0	43	24	ABK67415	Human 158p1H4 cDNA
C 43	27.8	1.0	43	24	ABL50410	Human 158p1F4 cDNA
C 44	27.8	1.0	43	24	ABL50412	DPNCDN cDNA synthe
C 45	27.8	1.0	43	24	AAS99436	

ALIGNMENTS

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DT	21-NOV-2001 (first entry)
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DE	Human reproductive system related antigen DNA SEQ ID NO: 10177.
XX	
KW	Human; reproductive system related antigen; reproductive system disorder;
KW	cancer; gene therapy; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200155320-A2.
XX	
PD	02-AUG-2001.
XX	
PF	17-JAN-2001; 2001WO-US01339.
XX	
PR	31-JAN-2000; 2000US-0179065.
PR	04-FEB-2000; 2000US-0180628.
PR	24-FEB-2000; 2000US-0184664.
PR	02-MAR-2000; 2000US-0186350.
PR	16-MAR-2000; 2000US-0189874.
PR	17-MAR-2000; 2000US-0190076.
PR	18-APR-2000; 2000US-0198123.
PR	19-MAY-2000; 2000US-0205515.
PR	07-JUN-2000; 2000US-0209467.
PR	28-JUN-2000; 2000US-0214886.
PR	30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
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PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
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PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
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PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
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PR 08-SEP-2000; 2000US-0231242.
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PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
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PR 25-SEP-2000; 2000US-0234997.
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PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
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PR 02-OCT-2000; 2000US-0236802.
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PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
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PR 20-OCT-2000; 2000US-0241787.

PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
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PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX
PI
XX
XX
DR
XX
XX
PT
PT
XX
PS
XX
CC
CC
CC
CC
CC
CC
XX
SQ
Sequence 47 BP; 36 A; 4 C; 2 G; 5 T; 0 other;
Query Match 1.1%; Score 31.4; DB 22; Length 47;

Isolated nucleic acid molecule encoding a reproductive system antigen
is used in preventing, treating or ameliorating a medical condition -
Disclosure; SEQ ID NO 10177; 1297pp + Sequence Listing; English.
The present invention provides the protein and coding sequences of a
number of human reproductive system related antigens. These can be used
in the prevention and treatment of reproductive system disorders,
including cancer. The present sequence is a genomic sequence encoding a
protein of the invention.


```
XX      WO9821332-A2.
PN      XX
XX      22-MAY-1998.
PD      XX
XX      14-NOV-1997; 97WO-US20740.
PF      XX
XX      13-NOV-1997; 97US-0969515.
PR      PR
XX      15-NOV-1996; 96US-0749745.
PR      PR
XX      02-JUN-1997; 97US-0867678.
XX      XX
PA      (GEMV ) GENETICS INST INC.
XX      XX
PI      Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
PI      Racie LA, Spaulding V, Treacy M;
XX      XX
DR      WPI; 1998-297936/26.
XX      XX
PT      New nucleic acid encoding secreted protein from human cells -
PT      potentially useful, e.g. as immuno-modulators, anti-tumour agents,
PT      promoters of tissue growth, haemostatic and thrombolytic agents
XX      XX
PS      Claim 24; Page 71; 98pp; English.
XX      XX
CC      This is the nucleotide sequence of the clone BD176_3, used in the
CC      method of the invention involving secreted proteins from human cells
CC      potentially useful as immuno-modulators, anti-tumour agents, tissue
CC      growth promoters, haemostatic and thrombolytic agents. It was isolated
CC      from a foetal human kidney cDNA library. They may be used to express
CC      the recombinant protein, as tissue/molecular weight markers, for
CC      chromosome identification, to identify possible genetic disorders and
CC      isolate new related DNA, as sources of primers for PCR, to generate
CC      anti-protein or anti-DNA antibodies, or in interaction trap assays to
CC      identify sequences that encode interacting proteins.
XX      XX
SQ      Sequence 49 BP; 44 A; 0 C; 1 G; 3 T; 1 other;

Query Match          1.1%; Score 30.4; DB 19; Length 49;
Best Local Similarity 75.5%; Pred. No. 3.4e+03;
Matches 37; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY      2151 TTGATTTTCTCCTTTTCTTTTCTTTTCTTTTAACTTTGAAGTT 2199
Db      49 TTTTCTTTTCTTATTTTCTTTTCTTTTCTTTTCTTTTNTTTAATTT 1

RESULT 5
AAF98419/C
ID      AAF98419 standard; cDNA; 49 BP.
XX      XX
AC      AAF98419;
XX      XX
DT      07-JUN-2001 (first entry)
XX      XX
DE      Human cDNA clone BD176_3 3' sequence SEQ ID 74.
XX      XX
KW      Human; secreted protein; nutrient; cytokine modulator; proliferation;
KW      differentiation; immune system modulator; tissue growth; chemotactic;
KW      haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;
KW      haematopoiesis.
XX      XX
OS      Homo sapiens.
XX      XX
PN      WO200119988-A1.
XX      XX
PD      22-MAR-2001.
XX      XX
PF      14-SEP-2000; 2000WO-US25135.
XX      XX
PR      17-SEP-1999; 99US-0398829.
XX      XX
PA      (GEMV ) GENETICS INST INC.
XX      XX
```

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PI      Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
PI      Merberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;
XX      XX
DR      WPI; 2001-244801/25.
XX      XX
PT      Isolated nucleic acids encoding polypeptides, useful for modulating
PT      e.g. cytokine and cell proliferation/differentiation activity, the
PT      immune system and hematopoiesis regulating activity -
XX      XX
PS      Disclosure; Page 429; 557pp; English.
XX      XX
CC      Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
CC      proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
CC      tissue types, and may be used in the prevention, treatment and diagnosis
CC      of diseases associated with inappropriate protein expression. The
CC      polypeptides and nucleic acids may be used as nutrients or to modulate
CC      cytokine and cell proliferation/differentiation activity and may also be
CC      involved in modulation of the immune system. The cDNA sequences,
CC      proteins, their agonists and/or antagonists exhibit haematopoiesis
CC      regulating activity; tissue growth activity; activin/inhibin activity;
CC      chemotactic/chemokinetic activity; haemostatic and thrombolytic
CC      activity; receptor/ligand activity; anti-inflammatory activity;
CC      haematopoiesis activity; cadherin/tumour suppressor activity; and/or
CC      tumour inhibition activity. Included in the invention are probes
CC      represented in AAF98490 - AAF98572 which are specific for the cDNA clones
CC      encoding the secreted proteins.
XX      XX
SQ      Sequence 49 BP; 44 A; 0 C; 1 G; 3 T; 1 other;

Query Match          1.1%; Score 30.4; DB 22; Length 49;
Best Local Similarity 75.5%; Pred. No. 3.4e+03;
Matches 37; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY      2151 TTGATTTTCTCCTTTTCTTTTCTTTTCTTTTAACTTTGAAGTT 2199
Db      49 TTTTCTTTTCTTATTTTCTTTTCTTTTCTTTTCTTTTNTTTAATTT 1

RESULT 6
AAS95724
ID      AAS95724 standard; DNA; 45 BP.
XX      XX
AC      AAS95724;
XX      XX
DT      14-FEB-2002 (first entry)
XX      XX
DE      Allele discrimination P1 primer #8.
XX      XX
KW      Rolling circle amplification; single nucleotide polymorphism; anaemia;
KW      exonuclease deficient DNA polymerase; amplification target circle; RCA;
KW      Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss;
KW      Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis;
KW      diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach;
KW      lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma;
KW      melanoma; PCR primer; sequencing primer; probe.
XX      XX
OS      Homo sapiens.
XX      XX
PN      WO200177390-A2.
XX      XX
PD      18-OCT-2001.
XX      XX
PF      05-APR-2001; 2001WO-US11151.
XX      XX
PR      05-APR-2000; 2000US-194843P.
XX      XX
PA      (MOLE-) MOLECULAR STAGING INC.
XX      XX
PI      Abarzua P;
XX      XX
DR      WPI; 2002-049157/06.
XX      XX
PT      Detecting single nucleotide polymorphism involves amplifying target
```

PT		sequences using small primer probe that matches or mismatches to target
PT		sequence and extending primer probe which is then detected -
XX		
XX		Claim 15; Page 41; 67pp; English.
CC		The invention relates to detecting single nucleotide polymorphisms by
CC		contacting an allele-specific oligonucleotide primer (P1) with a target
CC		polynucleotide to form a hybridisation complex, where the target sequence
CC		is complementary to P1 at one end but the terminal nucleotide and the
CC		third nucleotide from the terminal at the other end of P1 may not be
CC		complementary. The complex is then contacted with an exonuclease
CC		deficient DNA polymerase enzyme under conditions that promote extension
CC		of P1 with the target DNA as the template, thereby forming an extended
CC		segment of P1. Oligonucleotide probes hybridising to one or more target
CC		polynucleotides distinguish between matched and mismatched 3' ends, hence
CC		the absence of sequence amplification indicates the presence of a single
CC		nucleotide mismatch. Primer sequences complementary to a sequence on an
CC		amplification target circle can be used in rolling circle amplification
CC		(RCA). The method is useful for diagnosing a disease caused by, induced
CC		by or related to a mutation in at least one gene, such as Parkinson's
CC		disease, polycystic kidney disease, Tay-Sachs disease, Huntington
CC		disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes,
CC		obesity, cancers of the head, neck, skin, brain, oesophagus, stomach,
CC		lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma and
CC		melanoma. Sequences AAS95711-AAS95745 represent primers, targets and
CC		fluorescence decorators used in the detection of RCA products.
XX		
SQ		Sequence 45 BP; 1 A; 6 C; 0 G; 38 T; 0 other;
		Query Match 1.1%; Score 30; DB 24; Length 45;
		Best Local Similarity 86.8%; Pred. No. 4e+03;
		Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY		2155 TTTTCTCCTTTTTTTTTTTTTTTTACTTT 2192
Db		4 TTTTCTTTTTTTTTTTTTTTTTTTTCACCTT 41
RESULT 7		
AAS95728		ID AAS95728 standard; DNA; 45 BP.
XX AC		AAS95728;
XX DT		14-FEB-2002 (first entry)
DE XX		Allele discrimination P1 primer #12.
XX KW		Rolling circle amplification; single nucleotide polymorphism; anaemia;
KW KW		exonuclease deficient DNA polymerase; amplification target circle; RCA;
KW KW		Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss;
KW KW		Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis;
KW KW		diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach;
KW KW		lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma;
KW KW		melanoma; PCR primer; sequencing primer; probe.
XX OS		Homo sapiens.
XX PN		WO200177390-A2.
XX PD		18-OCT-2001.
XX PF		05-APR-2001; 2001WO-US11151.
XX PR		05-APR-2000; 2000US-194843P.
XX PA		(MOLE-) MOLECULAR STAGING INC.
PI PI		Abarzua P;
XX DR		WPI; 2002-049157/06.
XX PT		Detecting single nucleotide polymorphism involves amplifying target

[illegible]

OY 2151 TTGATTTTCTCCTTTTAACTTT 2192
|| ||||| | ||||| |||
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 42

RESULT 11
AAV09273/c
ID AAV09273 standard; cDNA; 44 BP.
XX
AC AAV09273;
XX
DT 07-JUL-1998 (first entry)
XX
DE Nucleotide sequence of the 3' portion of the BG513_19 protein.

XX
KW BG513_19 protein; human adult brain cDNA library; nutritional activity;
KW cytokine activity; cell proliferation/differentiation activity;
KW homology; ss.
XX
OS Homo sapiens.
XX
PN WO97448801-A2.
XX
PD 24-DEC-1997.
XX
PF 16-JUN-1997; 97WO-US10501.
XX
PR 17-JUN-1996; 96US-0664596.
XX
PA (GEMX) GENETICS INST INC.
XX
PI Bowman M, Evans C, Jacobs K, LaVallie ER, McCoy JM;
PI Merberg D, Racie LA, Spaulding V, Treacy M;
XX
DR WPI; 1998-063142/06.

XX
PT Poly:nucleotide(s) and proteins obtained from human PBMC, dendritic
PT cell, adult brain, foetal brain and adult testes cDNA libraries -
PT used in research, detection and therapy of, e.g. cytokine and cell
PT proliferation or differentiation
XX
PS Claim 19; Page 51; 78pp; English.
XX
CC This nucleotide sequence encodes the 3' portion of the BG513_19 protein
CC which was isolated from a human adult brain cDNA library. The products
CC of the polynucleotides of the invention can be used in research,
CC detection and therapy, as they may have nutritional activity, cytokine
CC and cell proliferation/differentiation activity. A search against the
CC Genbank database demonstrated that this sequence has no homology
CC with known sequences.

SQ Sequence 44 BP; 44 A; 0 C; 0 G; 0 U; 0 other;

Query Match 1.0%; Score 29.2; DB 19; Length 44;
Best Local Similarity 81.0%; Pred. No. 5.9e+03;
Matches 34; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 2151 TTGATTTTCTCCTTTTAACTTT 2192
|| ||||| | ||||| |||
Db 44 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 3

RESULT 12
AAT88080/c
ID AAT88080 standard; cDNA; 49 BP.
XX
AC AAT88080;

XX
DT 14-MAY-1998 (first entry)
XX
DE 3' portion of cDNA clone encoding secreted protein AK533.
XX
KW Human; secreted protein; research; treatment; AM533;

KW 3' portion; ds.
XX
OS Homo sapiens.
XX
PN WO9739122-A2.
XX
PD 23-OCT-1997.
XX
PF 11-APR-1997; 97WO-US06042.
XX
PR 12-APR-1996; 96US-0631184.
XX
PA (MURO-) MURO PHARM INC.
XX
PI Theoharides TC;
XX
DR WPI; 1997-526459/48.
XX
PT Human and murine secreted proteins - useful to research or treat
PT diseases or disorders related to their function
XX
PS Disclosure; Page 86; 140pp; English.

XX
CC The present sequence is the 3' portion of a cDNA clone encoding a
CC human secreted protein, which may have nutritional uses, or
CC cytokine and cell proliferation/differentiation, immune stimulating
CC or suppressing, haematopoiesis regulating, tissue growth,
CC activin/inhibin, chemotactic/chemokinetic, haemostatic and
CC thrombolytic, receptor/ligand, anti-inflammatory or tumour
CC inhibition activities. It can also be used to research or treat
CC diseases/disorders related to its function.
CC The partial cDNA clone AP162 was 1st isolated from a human adult
CC placenta cDNA library. The partial cDNA clones AM931, AM610, AM340,
CC AM282, AK647, AK583, AK533 and AK296 were 1st isolated from a human
CC foetal kidney cDNA library. The partial cDNA clones H617 and BB9
CC were 1st isolated from a human peripheral blood monocyte cell (Th1
CC or Th2) cDNA library. The partial cDNA clone AW191 was 1st isolated
CC from a human ovary (PA-1 teratocarcinoma) cDNA library. The partial
CC cDNA clones AT211, AT205 and AT319 were 1st isolated from a human
CC lymphocyte and dendritic cell cDNA library. The partial cDNA clones
CC AS34 and AS32 were 1st isolated from a human foetal brain cDNA
CC library. The partial cDNA clone AR260 was 1st isolated from a human
CC adult retina cDNA library. The partial cDNA clones K640 and K39
CC were 1st isolated from a murine bone marrow (stromal cell line
CC FCM-4) cDNA library.

SQ Sequence 49 BP; 40 A; 2 C; 6 G; 1 T; 0 other;

Query Match 1.0%; Score 29.2; DB 18; Length 49;
Best Local Similarity 81.0%; Pred. No. 6.2e+03;
Matches 34; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 2151 TTGATTTTCTCCTTTTAACTTT 2192
|| ||||| | ||||| |||
Db 48 TCGAGTTT TTTT TTTT TTTT TTTT TTTT TTTT 7

RESULT 13
AAV02146/c
ID AAV02146 standard; cDNA; 49 BP.
XX
AC AAV02146;

XX
DT 12-MAY-1998 (first entry)
XX
DE Human secreted protein AK533 3' portion including the polyA tail.
XX
KW Human; secreted protein; ATCC 98026; cytokine; immunomodulation;
XX cell proliferation; differentiation; regulation; ds.
XX
OS Homo sapiens.
XX
PN WO9739123-A2.

XX		23-OCT-1997.
PD		
XX	14-APR-1997;	97WO-US06139.
Pf		
XX	18-APR-1996;	96US-0634325.
PR		
XX	(GENE) GENETICS INST INC.	
PA		
XX	Jacobs K, Lavallie ER, McCoy JM, Merberg D, Racie LA; Spaulding V;	
PI		
PI		
DR	WPI; 1997-526460/48.	
XX		
PT	New secreted proteins encoded clones present in ATCC 98026 - possibly having cytokine, cell proliferation/differentiation regulating, immunomodulating and many other activities	
PS	Disclosure; Page 86; 139pp; English.	
XX		
CC	The present sequence encodes a portion of a novel human secreted protein deposited under accession number ATCC 98026. The secreted protein can be used to determine biological activity, to raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions and as nutritional supplements. It may also have a very wide range of biological activities although no evidence for any is provided in the specification. Typical of these are cytokine, cell proliferation/differentiation modulating activity or induction of other cytokines; immunostimulating/immunosuppressant activities (e.g. for treating human immunodeficiency virus infection, cancer, autoimmune diseases and allergy); regulation of haematopoiesis (e.g. for treating anaemia or as adjunct to chemotherapy); stimulation of growth of bone, cartilage, tendons, ligaments and/or nerves (e.g. for treating wounds, periodontal disease, neurological diseases stroke, fibrosis); inhibition or stimulation of follicle stimulating hormone (for control of fertility); chemotactic and chemokinetic activities (e.g. for treating infections, tumours); haemostatic or thrombolytic activity (e.g. for treating haemophilia, cardiac infarction etc.); anti-inflammatory activity (e.g. for treating psoriasis or other disease); as antimicrobials; for treating septic shock, Crohn's hyperproliferative disease; for regulating metabolism, behaviour, and many others. Also contemplated is the use of the corresponding nucleic acid in gene therapy procedures.	
CC		
CX	Sequence 49 BP; 40 A; 2 C; 6 G; 1 T; 0 other;	
SQ		
	Query Match	1.0%; Score 29.2; DB 18; Length 49;
	Best Local Similarity	81.0%; Pred. No. 6.2e+03;
	Matches 34; Conservative	0; Mismatches 8; Indels 0; Gaps 0;
OY	2151 TTGATTTTTCCTCCTTTTTTTTTTTTAACCTT 2192	
	I I	
Db	48 TCGAGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 7	
ID	AAQ66922 standard; DNA; 50 BP.	
XX		
AC	AAQ66922;	
XX		
DT	24-JAN-1995 (first entry)	
XX		
DE	Poly-da 50mer probe target sequence.	
XX		
Kw	Target sequence; binding ability; hairpin forming; probes;	
Kw	imperfect hairpin; acceptor label moiety; donor moiety label;	
Kw	fluoresence; fluorophores; specificity; base pair mismatches;	
Kw	competitive arms; ss.	
OS		
XX	Synthetic.	
Key		Location/Qualifiers

```

FT      misc_binding      2..26
FT      /tag= a
FT      /note= "Target sequence for probe binding"
XX      PN      EP601889-A.
XX      PD      15-JUN-1994.
XX      PF      10-DEC-1993;      93EP-0310007.
XX      PR      10-DEC-1992;      92US-0990298.
XX      PA      (MAIN-) MAINE MEDICAL CENT RES INST.
XX      PI      Bagwell BC;
XX      DR      WPI; 1994-185245/23.
XX      PT      Nucleic acid probe for use in DNA or RNA hybridisation assays -
XX      PT      comprises a nucleotide sequence which is capable of forming one
XX      PS      or more hairpins
XX      PS      Disclosure; Fig 2; 25pp; English.
XX      CC      This sequence represents a target sequence which was used to demonstrate
XX      CC      the binding ability of the hairpin forming probes of the invention. The
XX      CC      probes comprise a segment complementary to the target nucleotide and are
XX      CC      capable of forming at least 1 imperfect hairpin. The probes contain at
XX      CC      least one acceptor label moiety and at least one donor moiety label
XX      CC      which are covalently attached to the nucleotide sequence so that when
XX      CC      the hairpins are formed the moieties are in close proximity to allow
XX      CC      resonance energy transfer between them. This causes a reduction in the
XX      CC      fluorescence of the two fluorophores. The target sequence contains at
XX      CC      least 22 nucleotides to ensure specificity and avidity of the probe-
XX      CC      target hybridisation. The hairpins formed are imperfect hairpins and
XX      CC      the intentional base pair mismatches are introduced into the competitive
XX      CC      arms such that the specificity sequence will favour binding to the
XX      CC      target sequence. Therefore when the probe interacts with the target
XX      CC      sequence the competitive arm is displaced, increasing the distance
XX      CC      between the fluorophores, resulting in a change in fluorescent emission.
XX      SQ      Sequence 50 BP; 50 A; 0 C; 0 G; 0 T; 0 other;

Query Match      1.0%; Score 29.2; DB 15; Length 50;
Best local Similarity 81.0%; Pred. No. 6.2e+03;
Matches 34; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      2151 TTGATTTTTTCTCCCTTTTTTTTTTTTTTTTAACTTT 2192
      || ||||| | ||||| ||||| ||||| |||
DB      50 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 9

RESULT 15
ID      AAF60897 standard; DNA; 50 BP.
XX      AC      AAF60897;
XX      DT      15-MAY-2001 (first entry)
DE      Conjugate forming oligonucleotide ON6 SEQ ID 6.
KW      Transport; membrane; cytosstatic; virucide; vasotropic; dermatological;
KW      antiporiatic; antiasthmatic; gene therapy; tumor cell; antisense;
KW      tumor therapy; drug; phosphodiester linkage; ss.
XX      OS      Unidentified.
XX      PN      DE19935302-A1.
XX      PD      08-FEB-2001.
XX      PT      28-JUL-1999; 99DE-1035302.
XX      PF

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: APPLICATION NUMBER: US/08/439,996
: FILING DATE:
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/477,895A
: FILING DATE:
: APPLICATION NUMBER: US 08/128,583
: FILING DATE: 28-SEP-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Janluk, Anthony J
: REGISTRATION NUMBER: 29,809
: REFERENCE/DOCKET NUMBER: C0772/7004
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-720-3500
: TELEFAX: 617-720-2441
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 40 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: YES
:
US-08-439-996-4

```

Query	Match	1.08;	Score	28.4;	DB	3;	Length	40;	
	Best Local Similarity	84.2%;	Pred. No.	7e+02;					
Matches	32;	Conservative	0;	Mismatches	6;	Indels	0;	Gaps	0;
QY	2155	TTTTTTCCTCCTTTTTTTTTTTTTTTTAACTTT	2192						
Db	1	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	38						

```

RESULT 5
US-09-732-067-7/c
: Sequence 7, Application US/09732067
: Patent No. 6457426
: GENERAL INFORMATION:
: APPLICANT: Ullman, Edwin
: APPLICANT: Singh, Rajendra
: APPLICANT: Dekecezer, Steve
: APPLICANT: Davalian, Darlush
: TITLE OF INVENTION: Amplified Luminescent Homogeneous
: TITLE OF INVENTION: Immunoassay
: FILE REFERENCE: BEH-7385
: CURRENT APPLICATION NUMBER: US/09/732,067
: CURRENT FILING DATE: 2000-12-07
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 7
:   LENGTH: 40
:   TYPE: DNA
:   ORGANISM: Artificial Sequence
:   FEATURE:
:   OTHER INFORMATION: hybridization oligo
US-09-732-067-7

```

Query Match	1.0%;	Score 28.4;	DB 4;	Length 40;
Best Local Similarity	84.2%;	Pred. No. 7e+02;		
Matches 32; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0;
QY 2155	TTTTTTTCTCCCTTTT	TTTTTTTAACTTT	2192	
Ddb 40	TTTTTTTTTTTTTTTT	TTTTTTTTTTTTTTT	3	

RESULT 6
US-09-462-569B-4
; Sequence 4, Application US/09462569B
; Patent No. 6392124
; GENERAL INFORMATION:

```

; APPLICANT: PONZ ASCASO, Fernando
; APPLICANT: TORRES PASCUAL, Vicente
; APPLICANT: SANCHEZ SANCHEZ, Florentina
; APPLICANT: MARTINEZ HERRERA, David
; TITLE OF INVENTION: INFECTIOUS VECTORS AND CLONES OF PLANTS DERIVED FROM
; TITLE OF INVENTION: THE TURNIP MOSAIC VIRUS (TuMV)
; FILE REFERENCE: P/613-110
; CURRENT APPLICATION NUMBER: US/09/462,569B
; CURRENT FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: PCT/ES98/00200
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: ES P 9701522
; PRIOR FILING DATE: 1997-07-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
US-09-462-569B-4

```

	Query Match	1.0%;	Score 28;	DB 4;	length 36;	
	Best Local Similarity	86.1%;	Pred. No.	8.3e+02;		
	Matches	31;	Conservative	0;	Mismatches 5;	Indels 0;
Oy	2151	TTCGATTTTTTCTCCTTTTTTTTTTTTTTTT	2186			
Db	1	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	36			

```

RESULT 7
US-08-113-646A-44/c
; Sequence 44, Application US/08113646A
; Patent No. 5578468
; GENERAL INFORMATION:
; APPLICANT: PICKUP, David J.
; APPLICANT: PATEL, Dhaval Kumar
; APPLICANT: ANTCAK, James B.
; TITLE OF INVENTION: SITE-SPECIFIC RNA CLEAVAGE
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/113,646A
; FILING DATE: 31-AUG-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/084,406
; FILING DATE: 10-AUG-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs

```


us-10-023-782a-3.Lim50.rni

Page 5

	Query Match	1.08;	Score 27.4;	DB 1;	Length 50;
	Best Local Similarity	75.6%;	Pred. No. 1.3e+03;		
	Matches 34; Conservative	0;	Mismatches 11;	Indels 0;	Gaps 0;
OY	2142 GCCTGCTGATTGATTTTTCCTCTTTTTTTTTTTTTTTTTTTT				2186
Db	4 GCCGGAGCTCGAATTCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT				48

RESULT 11
US-08-286-304-5
Sequence 5, Application US/08286304
Patent No. 5571893
GENERAL INFORMATION:
APPLICANT: Baker, Joffre
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patln (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,304
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
ATTORNEY/AGENT INFORMATION:

```

; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 894P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEO ID NO: 5
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-286-304-5

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Query Match	Similarity	Score	DB 1;	length
Best Local	Similarity	75.68;	Pred. No. 1.3e+03;	
Matches	34;	Conservative	0;	Mismatches 11; Indels 0; Gaps 0;
QY	2142	GCCTGCTGATTGATTTTCTCTCTTTT	TTTTTTTTTTTTTTTTTTTT	2186
Db	4	GCCGCGAGCTCGAATTC	TTTTTTTTTTTTTTTTTTTT	48

```

RESULT 12
US-08-442-745-5
; Sequence 5, Application US/08442745
; Patent No. 5624806
;
GENERAL INFORMATION:
;
APPLICANT: Baker, Joffre
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
;
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,745
FILING DATE: 17-may-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286304
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 894P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-442-745-5

```


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us-10-023-782a-3.lim50.rni

Page 7

```

; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443.130
; FILING DATE: 17-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/233609
; FILING DATE: 25-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286304
; FILING DATE: 05-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: 894P1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8674
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-443-130-5

```

Query Match	1.0%;	Score 27.4;	DB 1;	Length 50;
Best Local Similarity	75.6%;	Pred. No. 1.3e+03;		
Matches 34; Conservative	0;	Mismatches 11;	Indels 0;	Gaps 0;

OY	2142	GCCCTGATGTGAATTTTTCCTTTTTTTTTTTTTTTTT	2186
Db	4	GCCCGAGCTCGAATCTTTTTTTTTTTTTTTTTTTTTTTT	48

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Search completed: March 3, 2003, 22:35:47
Job time : 103 secs
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; CURRENT APPLICATION NUMBER: US/09/827, 289
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: U.S. 60/194843
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: p1 primer for
; OTHER INFORMATION: use in allele discrimination
US-09-827-289-18

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Query Match	1.1%;	Score 30;	DB 10;	Length 45;
Best Local Similarity	86.8%;	Pred. No. 1e+03;		
Matches 33; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

[illegible]

```

RESULT 3
US-09-815-343-1012
; Sequence 1012, Application US/09815343
; Patent No. US20010055596A1
; GENERAL INFORMATION:
; APPLICANT: Meagher, Madeleine
; APPLICANT: Xu, Jiangchun
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.504
; CURRENT APPLICATION NUMBER: US/09/815,343
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1012
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-815-343-1012

```

Query Match	1.0%;	Score 29.2;	DB 10;	Length 50;
Best Local Similarity	81.0%;	Pred. No. 1.6e+03;		
Matches 34;	Conservative 0;	Mismatches 8;	Indels 0;	Gaps 0;

	Qy	2151 TTGATTTTCTCCCTTTTTTTTTTTTTTTTTTTAAACATT	2192
	Db	1 TTTTFTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	42

```

RESULT 4
US-09-827-289-21
; Sequence 21, Application US/09827289
; Patent No. US20020009716A1
; GENERAL INFORMATION:
; APPLICANT: Abarzua, Patricio
; TITLE OF INVENTION: Process for Allele Discrimination Using Primer
; TITLE OF INVENTION: Extension
; FILE REFERENCE: 469290-55
; CURRENT APPLICATION NUMBER: US/09/827, 289
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: U.S. 60/194843
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence

```

```

; FEATURE:
;
; OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
; OTHER INFORMATION: use in allele discrimination
US-09-827-289-21

```

Query Match	1.0%;	Score 29;	DB 10;	Length 46;
Best Local Similarity	86.5%;	Pred. No. 1.7e+03;		
Matches 32; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

[illegible]

```

RESULT 5
US-09-827-289-25      ; Sequence 25, Application US/09827289
                        ; Patent No. US20020009716A1
                        ; GENERAL INFORMATION:
                        ; APPLICANT: Abarzua, Patricio
                        ; TITLE OF INVENTION: Process for Allele Discrimination Using Primer
                        ; TITLE OF INVENTION: Extension
                        ; FILE REFERENCE: 469290-55
                        ; CURRENT APPLICATION NUMBER: US/09/827,289
                        ; CURRENT FILING DATE: 2001-04-05
                        ; PRIOR APPLICATION NUMBER: U.S. 60/194843
                        ; PRIOR FILING DATE: 2000-04-05
                        ; NUMBER OF SEQ ID NOS: 35
                        ; SOFTWARE: PatentIn Ver. 2.1
                        ; SEQ ID NO 25
                        ; LENGTH: 46
                        ; TYPE: DNA
                        ; ORGANISM: Artificial Sequence
                        ; FEATURE:
                        ; OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
US-09-827-289-25

```

Query Match	1.0%;	Score 29;	DB 10;	Length 46;
Best Local Similarity	86.5%;	Pred. No. 1.7e+03;		
Matches 32; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

	QY	2155	TGCTTTCCTCCCTTTCTTTTCTTTCTTTCTTTAACTCT	2191
	Db	1	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCATTT	37

```

RESULT 6
US-09-827-289-22
; Sequence 22, Application US/09827289
; Patent No. US20020009716A1
; GENERAL INFORMATION:
; APPLICANT: Abarzua, Patricio
; TITLE OF INVENTION: Process for Allele Discrimination Using Primer
; TITLE OF INVENTION: Extension
; FILE REFERENCE: 469290-55
; CURRENT APPLICATION NUMBER: US/09/827,289
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: U.S. 60/194843
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
US-09-827-289-22

```

Query Match	1.0%;	Score 28.4;	DB 10;	Length 46;
Best Local Similarity	84.28;	Pred. No. 2.3e+03;		

Matches	32;	Conservative	0;	Mismatches	6;	Indels	0;	Gaps	0;
QY	2155	TTTTTTCCTCTTTT	TTTTT	TTTTTTTAACTTT	2192				
Db	4	TTTTTTTTTTTTTT	TTTTTTTTTTTCTAT	41					

```

RESULT 7
US-09-827-289-26
; Sequence 26, Application US/09827289
; Patent No. US20020009716A1
; GENERAL INFORMATION:
; APPLICANT: Abarzua, Patricia
; TITLE OF INVENTION: Process for Allele Discrimination Using Primer
; TITLE OF INVENTION: Extension
; FILE REFERENCE: 469290-55
; CURRENT APPLICATION NUMBER: US/09/827, 289
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: U.S. 60/194843
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: P1 primer for
; US-09-827-289-26

```

	Query Match	1.0%;	Score 28.4;	DB 10;	Length 46;
	Best Local Similarity	84.2%;	Pred. No. 2.3e+03;		
	Matches 32;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;
QY	2155 TTTTTTCTCCATTTTCTTTTAACTTT	2192			
Ddb	4 TTTTTTTTTTTTTTTTTTTTTTCAT	41			

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RESULT 8
US-09-828-034-3/c
; Sequence 3, Application US/09828034
; Patent No. US20020064771A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Weidong
; APPLICANT: Hong, Zhi
; APPLICANT: Ferrari, Eric
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: IN01165
; CURRENT APPLICATION NUMBER: US/09/828, 034
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/195, 852
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-3

```

Query Match	1.08;	Score 28.2;	DB 10;	Length 36;
Best Local Similarity	90.9%;	Pred. No. 2.2e+03;		
Matches 30; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;
QY 2154	ATTTTCTCTCCCTTTT	TTTTTTTTTTTTTTTT	TTTTTT	2186
Db 36	ATTTT	TTTTTTTTTTTTTTTT	TTTTTTTTTTTT	4

```

RESULT 9
US-09-896-856-5
; Sequence 5, Application US/09896856
; Patent No. US20020137189A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Joffre
; Chien, Kenneth
; King, Kathleen
; Pennica, Diane
; Wood, William
; TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/896, 856
; FILING DATE: 29-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/733, 850
; FILING DATE: 18-OCT-1996
; APPLICATION NUMBER: US 08/471, 112
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: 08/233, 609
; FILING DATE: 25-APR-1994
; APPLICATION NUMBER: 08/286304
; FILING DATE: 05-AUG-1994
; APPLICATION NUMBER: 08/443129
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Conley, Deirdre L.
; REGISTRATION NUMBER: 36,487
; REFERENCE/DOCKET NUMBER: P0894P1D2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/952-2066
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-896-856-5

Query Match      1.0%; Score 27.4; DB 10; Length 50;
Best Local Similarity    75.6%; Pred. No. 3.9e+03;
Matches   34; Conservative    0; Mismatches   11; Indels     0; Gaps     0;

QY   2142 GCCTGCTGATTGATTTTTCCTCCCTTTTTTTTTTTTTTTTTTTT 2186
      ||| | | | | | | | | | | | | | | | | | | | | | | | |
Db    4 GCCGGAGAGCTCGAATCTCTTTTTTTTTTTTTTTTTTTTTTTTTTT 48

RESULT 10
US-09-828-034-2/c
; Sequence 2, Application US/09828034
; Patent No. US20020064771A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Weidong
; APPLICANT: Hong, Zhi
; APPLICANT: Ferrari, Eric

```


GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2003, 19:09:40 ; Search time 3815 Seconds
(without alignments)
11903.577 Million cell updates/sec

Title: US-10-023-782A-3
Perfect score: 2804
Sequence: 1 tcgcagagccgcgcgatgcgt.....gaaaaaaaaaaaaaaaaa 2804

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estlov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35.2	1.3	49	AI270095	AI270095 qt63c08.x
2	33.8	1.2	50	AA966391	AA966391 w4f01a1.r
3	33	1.2	49	AA116935	AA116935 mn22901.r
4	32.4	1.2	49	AI350847	AI350847 qt11e08.x
5	31.6	1.1	47	HSM002907	AI038431 Homo sapi
6	31.4	1.1	50	AA120437	AA120437 mn47a11.r

C	7	31.4	1.1	50	9	AA590944	AA590944 vm25f02.r
C	8	31.2	1.1	48	10	AV950753	AV950753 AV950753
C	9	31	1.1	46	2	HSM003158	AI038682 Homo sapi
C	10	31	1.1	49	2	HSM001347	AI037023 Homo sapi
C	11	31	1.1	49	9	AI431439	AI431439 th36h10.x
C	12	30.8	1.1	45	12	BF582680	BF582680 602094085
C	13	30.8	1.1	47	9	AL642997	AL642997 AL642997
C	14	30.8	1.1	47	10	AW250836	AW250836 2821228.3
C	15	30.8	1.1	49	9	AL048743	AL048743 DKFZp566K
C	16	30.8	1.1	50	13	BI491716	BI491716 df14b04.w
C	17	30.8	1.1	50	14	BQ256372	BQ256372 NISC_ko01
C	18	30.4	1.1	48	9	AL628936	AL628936 AL628936
C	19	30.4	1.1	49	9	AA254893	AA254893 m278d07.r
C	20	30.4	1.1	50	2	HSM009683	AI044833 Homo sapi
C	21	30.4	1.1	50	14	BQ393428	BQ393428 NISC_ng03
C	22	30.2	1.1	44	9	AL640163	AL640163 AL640163
C	23	30.2	1.1	45	10	AW249952	AW249952 2821663.3
C	24	30.2	1.1	46	2	HSM001086	AI036769 Homo sapi
C	25	30.2	1.1	47	2	HSM002960	AI038484 Homo sapi
C	26	30.2	1.1	50	9	AL587874	AL587874 AL587874
C	27	30	1.1	39	17	TA116F09P	AL462533 T. brucei
C	28	30	1.1	49	9	AA526728	AA526728 n191d10.s
C	29	30	1.1	49	12	BF343486	BF343486 602017592
C	30	30	1.1	49	13	BI090256	BI090256 602855121
C	31	30	1.1	49	13	BI858831	BI858831 603388748
C	32	30	1.1	49	17	AZ587341	AZ587341 IM0394020
C	33	30	1.1	50	2	HSM002946	AI038470 Homo sapi
C	34	30	1.1	50	10	AW333255	AW333255 S19D3 AGS
C	35	30	1.1	50	12	BG256941	BG256941 602370419
C	36	30	1.1	50	13	BI493940	BI493940 df106e06.
C	37	30	1.1	50	14	BQ265586	BQ265586 NISC_ff07
C	38	29.8	1.1	50	9	AL641164	AL641164 AL641164
C	39	29.8	1.1	50	9	AA564185	AA564185 n104d11.s
C	40	29.6	1.1	36	12	BE894682	BE894682 601435925
C	41	29.6	1.1	38	17	AZ773771	AZ773771 2M0001B04
C	42	29.6	1.1	44	12	BG117508	BG117508 602347636
C	43	29.6	1.1	45	9	AL587540	AL587540 AL587540
C	44	29.6	1.1	45	12	BF525658	BF525658 602069777
C	45	29.6	1.1	45	17	AZ467950	AZ467950 IM0279L07

ALIGNMENTS

RESULT 1
AI270095 LOCUS 49 bp mRNA linear EST 17-NOV-1998
DEFINITION qt63c08.x1 NCI_CGAP_Eso2 Homo sapiens CDNA clone IMAGE:1959950 3',
ACCESSION AI270095
VERSION AI270095.1 GI:3889262
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE 1 (bases 1 to 49)
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Nan Hu, M.D., Ph.D., Mark Roth, M.D., Phillip Taylor, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.

FEATURES

Location/Qualifiers

	Query Match	1.18;	Score 31;	DB 2;	Length 46;
	Best Local Similarity	87.2%;	Pred. No. 1.6e+06;		
	Matches 34;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;
QY	2151 TTGATTTCCTCCTTTT	TTTTTTTTTTTTTTT	TTTAAAC	2189	
Db	41 TTTTTCCTTCCTTTT	TTTTTTTTTTTTTTT	TTTAAAC	3	

SEQ	Sequence	49 BP; 39 A; 0 C; 8 G; 2 T; 0 other;
QY	Query Match	1.1%; Score 31; DB 2; Length 49;
	Best Local Similarity	87.2%; Pred. No. 1.5e+06;
	Matches	34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Db	2151 TTGATTTTTTCTCCTTTTTTTTTTTTTTTTAAAC	2189
	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAC	8
RESULT 11		
LOCUS	AI431439	49 bp mRNA linear EST 09-MAR-1999
DEFINITION	th36h10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2120419 3'	
ACCESSION	AI431439	similar to contains Alu repetitive element;; mRNA sequence.
VERSION	AI431439.1	GI:4303194
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 49)	
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	Tumor Gene Index	
JOURNAL	Unpublished (1997)	
COMMENT	Contact: Robert Strausberg, Ph.D.	
	Email: cgapbs-r@mail.nih.gov	
	Life Technologies catalog #: 11548-013	
	DNA Sequencing by: Washington University Genome Sequencing Center	
	Clone distribution: NCI-CGAP clone distribution information can be	
	found through the I.M.A.G.E. Consortium/BLNL at:	
	www.bio.llnl.gov/bbrp/image/image.html	
	Seq primer: -40UP from Gibco.	
FEATURES	Location/Qualifiers	
source	1..49	
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/clone="IMAGE:2120419"	
	/clone_lib="NCI_CGAP_Pan1"	
	/tissue_type="adenocarcinoma"	
	/lab_host="DH10B"	
	/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;	
	Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.	
	Average insert size 1.72 kb. Life Technologies catalog #:	
	11548-013"	
BASE COUNT	4 a 0 c 1 g 44 t	
ORIGIN		
Query Match	1.1%; Score 31; DB 9; Length 49;	
Best Local Similarity	78.7%; Pred. No. 1.5e+06;	
Matches	37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;	
QY	2151 TTGATTTTTTCTCCTTTTTTTTTTTTAACTTGAAG	2197
	TTTTTTTTTTTTTTTTTTTTTTTTTTTATAG	47
Db	1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATAG	47
RESULT 12		
LOCUS	BF582680	45 bp mRNA linear EST 12-DEC-2000
DEFINITION	602094085F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4208373 5',	
ACCESSION	BF582680	mRNA sequence.
VERSION	BF582680.1	GI:11656398
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus	

